

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/824,575A  
Source: 1600  
Date Processed by STIC: 1/11/05

# ***ENTERED***

RECEIVED

NOV 14 2005

TECH CENTER 1600/2900



1600

## RAW SEQUENCE LISTING

DATE: 01/11/2005

PATENT APPLICATION: US/09/824,575A

TIME: 17:44:11

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\01112005\I824575A.raw

4 <110> APPLICANT: BEASLEY, Ellen M. et al  
6 <120> TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
7 NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
8 AND USES THEREOF  
10 <130> FILE REFERENCE: CL000998  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/824,575A  
C--> 12 <141> CURRENT FILING DATE: 2001-04-03  
12 <160> NUMBER OF SEQ ID NOS: 4  
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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17 <211> LENGTH: 3487  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Human  
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24 ggatcagtac ggccaagtac agcgtgttga cttttctacc tcgattcttg tatgagcaga 180  
25 ttagaagagc tgctaattgcc ttctttctct tcattgcctt attacagcaa attccagatg 240  
26 tatctccaac aggaagatat accaccctgg tgccattgat cattatttta acaattgcag 300  
27 gcatcaaaga gattgtagaa gattttaagc gacacaaggc agacaatgca gttaacaaaa 360  
28 agaaaacaat agtgtaaga aatggtatgt ggcataccat tatgtggaaa gaggtggcag 420  
29 tgggagacat tgtgaaggtc gtcaatgggc agtatcttcc agcagatgtg gtcctgctgt 480  
30 catccagtga acctcaggca atgtgttatg ttgaaacagc taatctggat ggggagacga 540  
31 accttaaaat acgtcagggt ttgagtcaca ctgctgacat gcaaacacgt gaagtctga 600  
32 tgaagtatatc tggaaactata gagtgtgaag ggcccaaccg ccacctctat gacttactg 660  
33 gaaacttgaa cttagatggg aaaagccttg ttgcccttgg gcctgaccag atcttattaa 720  
34 gaggtacaca gcttagaaat actcagtggg tctttggcat agttgtttat actggacacg 780  
35 acaccaaact catgcagaat tcaaccaaaag cgctctcaa gagatcaaat gttgagaagg 840  
36 tgactaacgt gcagatcctg gtgttgtttg gcatcctctt ggtcatggcc ttggtgagct 900  
37 cggcgggggc cctgtactgg aacaggtctc atggtgaaaa gaactggtac atcaagaaga 960  
38 tggacaccac ctacagataat tttggataca acctactgac gttcatcatc ttatacaaca 1020  
39 atcttattcc catcagtctg ttggtgactc ttgaggttgt gaagtatact caagcccttt 1080  
40 tcataaactg ggacacagat atgtattata taggaaatga cactcctgcc atggccagga 1140  
41 catcaaacct taatgaagag cttgggcagg tgaaatatct cttttctgac aagactggaa 1200  
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43 acttcccaga attggcaaga gagccgtctt cagatgactt ctgtcggatg cctcctccct 1320  
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45 ccacagcccc ttgcattcag gagttcctca cccttctggc cgtgtgccac acggttggtc 1440  
46 ctgagaagga tggagataac atcatctacc aggcctcttc cccagatgaa gctgcttttg 1500  
47 tgaaaggagc taaaaagctg ggctttgtct tcacagccag aacaccattc tcagtcatca 1560  
48 tagaagcgat gggacaggaa caaacatttg gaatccttaa tgtcctggaa ttttctagt 1620  
49 acagaaaaag aatgtctgta attgttcgaa ctcttcagg acgacttcgg ctttactgta 1680  
50 aaggggctga taatgtgatt tttgagagac tttcaaaaga ctcaaaatat atggaggaaa 1740

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52 ctgatctctc tgagaatgag tatgaggagt ggctgaaagt ctatcaggaa gccagcacca 1860
53 tattgaagga cagagctcaa cggttggaag agtgttacga gatcattgag aagaatttgc 1920
54 tgctacttgg agccacagcc atagaagatc gccttcaagc aggagttcca gaaaccatcg 1980
55 caacactggt gaaggcagaa attaaaatat ggggtgttgac aggagacaaa caagaaactg 2040
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58 atttgctggg caaggaaaat gacgtggccc tcatcatcga tggccacacc ctgaagtacg 2220
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60 tatgctgcag agtgtctcct ctgcagaagt ctgagatagt ggatgtggtg aagaagcggg 2340
61 tgaaggccat caccctcgcc atcggagacg gcgccaacga tgcgggatg atccagacag 2400
62 cccacgtggg tgtgggaatc agtgggaatg aaggcatgca ggccaccaac aactcggatt 2460
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66 gcatcggcct gtacaatgtg attttcaccg ctttgccgcc cttcactctg ggaatctttg 2700
67 agaggctctg cactcaggag agcatgctca ggtttcccca gctctacaaa atcaccaga 2760
68 atggcggaag cttcaacaca aaggttttct ggggtcactg catcaacgcc ttggtccact 2820
69 cctcatcctt cttctggttt cccatgaaag ctctggagca tgatactgtg ttgacaagtg 2880
70 gtcatgctac cgactattta tttgttgga atattgttta cacatatgtt gttgttactg 2940
71 tttgtctgaa agctgggttg gagaccacag cttggactaa attcagtcac ctggctgtct 3000
72 ggggaagcat gctgacctgg ctgggtgttt ttggcatcta ctgaccatc tggcccacca 3060
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74 gggtgggatt atttctggtt cctactgcct gtttgattga agatgtggca tggagagcag 3180
75 ccaagcacac ctgcaaaaag acattgccgg aggaggtgca ggagctggaa accaagtctc 3240
76 gagtcctggg aaaagcgggt ctgcgggata gcaatggaaa gaggtgaac gagcgcgacc 3300
77 gcctgatcaa gaggccgggc cggaagacgc ccccgacgct gttccggggc agctccctgc 3360
78 agcagggcgt cccgcatggg tatgcttttt ctcaagaaga acacggagct gttagtcagg 3420
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82 &lt;210&gt; SEQ ID NO: 2

83 &lt;211&gt; LENGTH: 1148

84 &lt;212&gt; TYPE: PRT

85 &lt;213&gt; ORGANISM: Human

87 &lt;400&gt; SEQUENCE: 2

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89 1 5 10 15
90 Thr Ile Tyr Leu Asn Gln Pro His Leu Asn Lys Phe Arg Asp Asn Arg
91 20 25 30
92 Ile Ser Thr Ala Lys Tyr Ser Val Leu Thr Phe Leu Pro Arg Phe Leu
93 35 40 45
94 Tyr Glu Gln Ile Arg Arg Ala Ala Asn Ala Phe Phe Leu Phe Ile Ala
95 50 55 60
96 Leu Leu Gln Gln Ile Pro Asp Val Ser Pro Thr Gly Arg Tyr Thr Thr
97 65 70 75 80
98 Leu Val Pro Leu Ile Ile Ile Leu Thr Ile Ala Gly Ile Lys Glu Ile
99 85 90 95
100 Val Glu Asp Phe Lys Arg His Lys Ala Asp Asn Ala Val Asn Lys Lys
101 100 105 110

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102 Lys Thr Ile Val Leu Arg Asn Gly Met Trp His Thr Ile Met Trp Lys
103      115      120      125
104 Glu Val Ala Val Gly Asp Ile Val Lys Val Val Asn Gly Gln Tyr Leu
105      130      135      140
106 Pro Ala Asp Val Val Leu Leu Ser Ser Ser Glu Pro Gln Ala Met Cys
107 145      150      155      160
108 Tyr Val Glu Thr Ala Asn Leu Asp Gly Glu Thr Asn Leu Lys Ile Arg
109      165      170      175
110 Gln Gly Leu Ser His Thr Ala Asp Met Gln Thr Arg Glu Val Leu Met
111      180      185      190
112 Lys Leu Ser Gly Thr Ile Glu Cys Glu Gly Pro Asn Arg His Leu Tyr
113      195      200      205
114 Asp Phe Thr Gly Asn Leu Asn Leu Asp Gly Lys Ser Leu Val Ala Leu
115      210      215      220
116 Gly Pro Asp Gln Ile Leu Leu Arg Gly Thr Gln Leu Arg Asn Thr Gln
117 225      230      235      240
118 Trp Val Phe Gly Ile Val Val Tyr Thr Gly His Asp Thr Lys Leu Met
119      245      250      255
120 Gln Asn Ser Thr Lys Ala Pro Leu Lys Arg Ser Asn Val Glu Lys Val
121      260      265      270
122 Thr Asn Val Gln Ile Leu Val Leu Phe Gly Ile Leu Leu Val Met Ala
123      275      280      285
124 Leu Val Ser Ser Ala Gly Ala Leu Tyr Trp Asn Arg Ser His Gly Glu
125      290      295      300
126 Lys Asn Trp Tyr Ile Lys Lys Met Asp Thr Thr Ser Asp Asn Phe Gly
127 305      310      315      320
128 Tyr Asn Leu Leu Thr Phe Ile Ile Leu Tyr Asn Asn Leu Ile Pro Ile
129      325      330      335
130 Ser Leu Leu Val Thr Leu Glu Val Val Lys Tyr Thr Gln Ala Leu Phe
131      340      345      350
132 Ile Asn Trp Asp Thr Asp Met Tyr Tyr Ile Gly Asn Asp Thr Pro Ala
133      355      360      365
134 Met Ala Arg Thr Ser Asn Leu Asn Glu Glu Leu Gly Gln Val Lys Tyr
135      370      375      380
136 Leu Phe Ser Asp Lys Thr Gly Thr Leu Thr Cys Asn Ile Met Asn Phe
137 385      390      395      400
138 Lys Lys Cys Ser Ile Ala Gly Val Thr Tyr Gly His Phe Pro Glu Leu
139      405      410      415
140 Ala Arg Glu Pro Ser Ser Asp Asp Phe Cys Arg Met Pro Pro Pro Cys
141      420      425      430
142 Ser Asp Ser Cys Asp Phe Asp Asp Pro Arg Leu Leu Arg Asn Ile Glu
143      435      440      445
144 Asp Arg His Pro Thr Ala Pro Cys Ile Gln Glu Phe Leu Thr Leu Leu
145      450      455      460
146 Ala Val Cys His Thr Val Val Pro Glu Lys Asp Gly Asp Asn Ile Ile
147 465      470      475      480
148 Tyr Gln Ala Ser Ser Pro Asp Glu Ala Ala Leu Val Lys Gly Ala Lys
149      485      490      495
150 Lys Leu Gly Phe Val Phe Thr Ala Arg Thr Pro Phe Ser Val Ile Ile

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151		500		505		510
152	Glu Ala Met Gly Gln Glu Gln Thr Phe Gly Ile Leu Asn Val Leu Glu					
153		515		520		525
154	Phe Ser Ser Asp Arg Lys Arg Met Ser Val Ile Val Arg Thr Pro Ser					
155		530		535		540
156	Gly Arg Leu Arg Leu Tyr Cys Lys Gly Ala Asp Asn Val Ile Phe Glu					
157	545		550		555	560
158	Arg Leu Ser Lys Asp Ser Lys Tyr Met Glu Glu Thr Leu Cys His Leu					
159		565		570		575
160	Glu Tyr Phe Ala Thr Glu Gly Leu Arg Thr Leu Cys Val Ala Tyr Ala					
161		580		585		590
162	Asp Leu Ser Glu Asn Glu Tyr Glu Glu Trp Leu Lys Val Tyr Gln Glu					
163		595		600		605
164	Ala Ser Thr Ile Leu Lys Asp Arg Ala Gln Arg Leu Glu Glu Cys Tyr					
165		610		615		620
166	Glu Ile Ile Glu Lys Asn Leu Leu Leu Leu Gly Ala Thr Ala Ile Glu					
167	625		630		635	640
168	Asp Arg Leu Gln Ala Gly Val Pro Glu Thr Ile Ala Thr Leu Leu Lys					
169		645		650		655
170	Ala Glu Ile Lys Ile Trp Val Leu Thr Gly Asp Lys Gln Glu Thr Ala					
171		660		665		670
172	Ile Asn Ile Gly Tyr Ser Cys Arg Leu Val Ser Gln Asn Met Ala Leu					
173		675		680		685
174	Ile Leu Leu Lys Glu Asp Ser Leu Asp Ala Thr Arg Ala Ala Ile Thr					
175		690		695		700
176	Gln His Cys Thr Asp Leu Gly Asn Leu Leu Gly Lys Glu Asn Asp Val					
177	705		710		715	720
178	Ala Leu Ile Ile Asp Gly His Thr Leu Lys Tyr Ala Leu Ser Phe Glu					
179		725		730		735
180	Val Arg Arg Ser Phe Leu Asp Leu Ala Leu Ser Cys Lys Ala Val Ile					
181		740		745		750
182	Cys Cys Arg Val Ser Pro Leu Gln Lys Ser Glu Ile Val Asp Val Val					
183		755		760		765
184	Lys Lys Arg Val Lys Ala Ile Thr Leu Ala Ile Gly Asp Gly Ala Asn					
185		770		775		780
186	Asp Val Gly Met Ile Gln Thr Ala His Val Gly Val Gly Ile Ser Gly					
187	785		790		795	800
188	Asn Glu Gly Met Gln Ala Thr Asn Asn Ser Asp Tyr Ala Ile Ala Gln					
189		805		810		815
190	Phe Ser Tyr Leu Glu Lys Leu Leu Leu Val His Gly Ala Trp Ser Tyr					
191		820		825		830
192	Asn Arg Val Thr Lys Cys Ile Leu Tyr Cys Phe Tyr Lys Asn Val Val					
193		835		840		845
194	Leu Tyr Ile Ile Glu Leu Trp Phe Ala Phe Val Asn Gly Phe Ser Gly					
195		850		855		860
196	Gln Ile Leu Phe Glu Arg Trp Cys Ile Gly Leu Tyr Asn Val Ile Phe					
197	865		870		875	880
198	Thr Ala Leu Pro Pro Phe Thr Leu Gly Ile Phe Glu Arg Ser Cys Thr					
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201          900          905          910
202 Gly Glu Gly Phe Asn Thr Lys Val Phe Trp Gly His Cys Ile Asn Ala
203          915          920          925
204 Leu Val His Ser Leu Ile Leu Phe Trp Phe Pro Met Lys Ala Leu Glu
205          930          935          940
206 His Asp Thr Val Leu Thr Ser Gly His Ala Thr Asp Tyr Leu Phe Val
207 945          950          955          960
208 Gly Asn Ile Val Tyr Thr Tyr Val Val Val Thr Val Cys Leu Lys Ala
209          965          970          975
210 Gly Leu Glu Thr Thr Ala Trp Thr Lys Phe Ser His Leu Ala Val Trp
211          980          985          990
212 Gly Ser Met Leu Thr Trp Leu Val Phe Phe Gly Ile Tyr Ser Thr Ile
213          995          1000          1005
214 Trp Pro Thr Ile Pro Ile Ala Pro Asp Met Arg Gly Gln Ala Thr Met
215          1010          1015          1020
216 Val Leu Ser Ser Ala His Phe Trp Leu Gly Leu Phe Leu Val Pro Thr
217 1025          1030          1035          1040
218 Ala Cys Leu Ile Glu Asp Val Ala Trp Arg Ala Ala Lys His Thr Cys
219          1045          1050          1055
220 Lys Lys Thr Leu Pro Glu Glu Val Gln Glu Leu Glu Thr Lys Ser Arg
221          1060          1065          1070
222 Val Leu Gly Lys Ala Val Leu Arg Asp Ser Asn Gly Lys Arg Leu Asn
223          1075          1080          1085
224 Glu Arg Asp Arg Leu Ile Lys Arg Pro Gly Arg Lys Thr Pro Pro Thr
225          1090          1095          1100
226 Leu Phe Arg Gly Ser Ser Leu Gln Gln Gly Val Pro His Gly Tyr Ala
227 1105          1110          1115          1120
228 Phe Ser Gln Glu Glu His Gly Ala Val Ser Gln Glu Glu Val Ile Arg
229          1125          1130          1135
230 Ala Tyr Asp Thr Thr Lys Lys Lys Ser Arg Lys Lys
231          1140          1145
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 559686
236 <212> TYPE: DNA
237 <213> ORGANISM: Human
239 <220> FEATURE:
240 <221> NAME/KEY: misc_feature
241 <222> LOCATION: (1)...(559686)
242 <223> OTHER INFORMATION: n = A,T,C or G
244 <400> SEQUENCE: 3
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246 cactggtaag taaccatggt tacaccttta tgccttaatt gaggaacat tttcaagggc 120
247 aggaacctga tcttctgttt ttgtgttctc agcggcatct aacaagtgat cctgactggg 180
248 tgctcatcag catcacttag tgatctttag aagcaaaaca cagtgaccac agaactctgag 240
249 agggcagggc ccgggaacta atacattgtg gaagctgcat tggtataact aatgcacagg 300
250 ggaactgaga gccgctaggt gagcaatgaa ccactttgac cagcactgt tcagtgaacc 360
251 cagcctgtcc ctactgtcct ggagcttggg cttctgggtg cagtgaagaca gagcatccat 420
252 aaataaaatc aggtaatgat gatatctggt actgtggagg aagacaaggc aggggttagtg 480

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Output Set: N:\CRF4\01112005\I824575A.raw

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## VERIFICATION SUMMARY

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TIME: 17:44:12

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\01112005\I824575A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:921 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:40560

M:341 Repeated in SeqNo=3